

=====

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=27; hr=18; min=57; sec=54; ms=523;]

=====

Application No: 10587067 Version No: 1.1

Input Set:

Output Set:

Started: 2008-08-27 18:54:59.956
Finished: 2008-08-27 18:55:01.976
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 20 ms
Total Warnings: 0
Total Errors: 0
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

SEQUENCE LISTING

<110> VERMEIJ, Paul

<120> Lawsonia Intracellularis Subunit Vaccines

<130> I-2004.001 US

<140> 10587067

<141> 2008-08-23

<150> PCT/EP2005/000562

<151> 2005-01-18

<150> EP 04100202.3

<151> 2004-01-22

<150> EP 04100203.1

<151> 2004-01-22

<150> EP 04100204.9

<151> 2004-01-22

<150> EP 04100205.6

<151> 2004-01-22

<150> EP 04100206.4

<151> 2004-01-22

<150> EP 04100208.0

<151> 2004-01-22

<150> EP 04100209.8

<151> 2004-01-22

<150> EP 04100210.6

<151> 2004-01-22

<150> EP 04100211.4

<151> 2004-01-22

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 2088

<212> DNA

<213> Lawsonia intracellularis

<220>

<221> CDS

<222> (16)..(2085)

<400> 1

cggaggttga ttact atg agt ctt aca gca gga atg tgg aca ggt gtt tca

Met Ser Leu Thr Ala Gly Met Trp Thr Gly Val Ser																			
				1					5					10					
gga	ctt	tta	agt	cat	ggc	gaa	aag	atg	aat	gtt	att	ggg	aat	aac	ata	99			
Gly	Leu	Leu	Ser	His	Gly	Glu	Lys	Met	Asn	Val	Ile	Gly	Asn	Asn	Ile				
15						20						25							
gct	aac	gta	aat	aca	gta	ggc	ttt	aaa	ggc	caa	cgt	atg	gat	ttc	gca	147			
Ala	Asn	Val	Asn	Thr	Val	Gly	Phe	Lys	Gly	Gln	Arg	Met	Asp	Phe	Ala				
30						35						40							
gac	ttt	att	tat	caa	gat	ggc	ttt	agt	act	gca	ggg	att	aca	caa	att	195			
Asp	Phe	Ile	Tyr	Gln	Asp	Gly	Phe	Ser	Thr	Ala	Gly	Ile	Thr	Gln	Ile				
45						50						55			60				
gga	cgt	ggg	gta	ggc	att	gga	gct	gtc	atg	ggg	aac	ttt	ggg	cag	ggg	243			
Gly	Arg	Gly	Val	Gly	Ile	Gly	Ala	Val	Met	Gly	Asn	Phe	Gly	Gln	Gly				
				65						70						75			
agt	ttt	gaa	acc	aca	act	gaa	gca	aca	gac	ctt	gct	att	ggg	ggg	cgt	291			
Ser	Phe	Glu	Thr	Thr	Thr	Glu	Ala	Thr	Asp	Leu	Ala	Ile	Gly	Gly	Arg				
			80						85						90				
gga	ttt	ttc	aaa	gtt	aaa	cca	caa	gga	tca	gag	act	tca	tat	tat	acc	339			
Gly	Phe	Phe	Lys	Val	Lys	Pro	Gln	Gly	Ser	Glu	Thr	Ser	Tyr	Tyr	Thr				
95						100						105							
cgt	gca	ggg	aat	ttt	cgt	ttt	aat	aat	gat	gga	tac	tta	gtt	gat	cct	387			
Arg	Ala	Gly	Asn	Phe	Arg	Phe	Asn	Asn	Asp	Gly	Tyr	Leu	Val	Asp	Pro				
110						115						120							
cat	gga	tat	gct	ctt	cag	ggg	tgg	aaa	att	gat	aat	act	gaa	ggg	cca	435			
His	Gly	Tyr	Ala	Leu	Gln	Gly	Trp	Lys	Ile	Asp	Asn	Thr	Glu	Gly	Pro				
125							130						135			140			
caa	cgt	atc	tca	ggg	ggg	gtt	aat	cca	ggg	aca	aat	act	tcg	cag	att	483			
Gln	Arg	Ile	Ser	Gly	Gly	Val	Asn	Pro	Gly	Thr	Asn	Thr	Ser	Gln	Ile				
				145						150						155			
atg	ggg	aca	ggg	gaa	cca	aca	gat	atc	cgt	ctt	gat	act	tgg	aca	gtt	531			
Met	Gly	Thr	Gly	Glu	Pro	Thr	Asp	Ile	Arg	Leu	Asp	Thr	Trp	Thr	Val				
			160						165						170				
gca	cct	tta	cag	aca	aca	aat	gta	agt	ttt	aac	gta	aac	ctt	tct	tct	579			
Ala	Pro	Leu	Gln	Thr	Thr	Asn	Val	Ser	Phe	Asn	Val	Asn	Leu	Ser	Ser				
175						180						185							
gat	aaa	tct	gga	gat	aaa	tct	caa	aac	gtt	aat	agt	cca	ttt	acc	tca	627			
Asp	Lys	Ser	Gly	Asp	Lys	Ser	Gln	Asn	Val	Asn	Ser	Pro	Phe	Thr	Ser				
190						195						200							
tta	ttt	aat	ata	tgg	aat	ggg	aaa	caa	cca	agt	gaa	cct	aac	aat	cca	675			
Leu	Phe	Asn	Ile	Trp	Asn	Gly	Lys	Gln	Pro	Ser	Glu	Pro	Asn	Asn	Pro				
205					210						215						220		
cct	atg	cct	gaa	agt	gca	tat	agt	tat	cag	aca	tct	att	aag	gta	tat	723			
Pro	Met	Pro	Glu	Ser	Ala	Tyr	Ser	Tyr	Gln	Thr	Ser	Ile	Lys	Val	Tyr				

	225		230		235	
	gat gaa gct ggt gga aca cat aca tta aca gtc tat ttt gac caa gtt					771
	Asp Glu Ala Gly Gly Thr His Thr Leu Thr Val Tyr Phe Asp Gln Val					
	240		245		250	
	tct cct aaa gac tac aaa ggt ggt gga agt gga gaa agt gta tgg gaa					819
	Ser Pro Lys Asp Tyr Lys Gly Gly Gly Ser Gly Glu Ser Val Trp Glu					
	255		260		265	
	tac gtt gtt act atg gat cct tct gaa gat aat cgc caa gtt tct gtt					867
	Tyr Val Val Thr Met Asp Pro Ser Glu Asp Asn Arg Gln Val Ser Val					
	270		275		280	
	ggt ggt aac att gtg gac atc aaa gat act aaa gct gca gga atg tta					915
	Gly Gly Asn Ile Val Asp Ile Lys Asp Thr Lys Ala Ala Gly Met Leu					
	285		290		295	300
	atg tca gga aca ttg agt ttt gat agc tca gga aaa ctt gca aac caa					963
	Met Ser Gly Thr Leu Ser Phe Asp Ser Ser Gly Lys Leu Ala Asn Gln					
	305		310		315	
	agt gca tat tcg ctg aat ggt tca cgt aag cct gca gtt gat cct gca					1011
	Ser Ala Tyr Ser Leu Asn Gly Ser Arg Lys Pro Ala Val Asp Pro Ala					
	320		325		330	
	acc gga gct ctt att aat ggt aat ggt ttt act att gat aga gat gga					1059
	Thr Gly Ala Leu Ile Asn Gly Asn Gly Phe Thr Ile Asp Arg Asp Gly					
	335		340		345	
	aat gca att cct att ctt aat ata gat aat cca gct gaa aac ttc tat					1107
	Asn Ala Ile Pro Ile Leu Asn Ile Asp Asn Pro Ala Glu Asn Phe Tyr					
	350		355		360	
	cca gca gaa gtt tct aat aat gga ttt cct atg att gta gct aat ttt					1155
	Pro Ala Glu Val Ser Asn Asn Gly Phe Pro Met Ile Val Ala Asn Phe					
	365		370		375	380
	act ggt gtc cca ggt aaa aat aca gct gga tct gtt ggt gat gct acc					1203
	Thr Gly Val Pro Gly Lys Asn Thr Ala Gly Ser Val Gly Asp Ala Thr					
	385		390		395	
	acc ttt ttt aca gaa att gac ttt ggt tta aaa gct act gat ctt gat					1251
	Thr Phe Phe Thr Glu Ile Asp Phe Gly Leu Lys Ala Thr Asp Leu Asp					
	400		405		410	
	aat aca tgg aag aat gca aat gaa cct ctt tct tct tta agc tat aaa					1299
	Asn Thr Trp Lys Asn Ala Asn Glu Pro Leu Ser Ser Leu Ser Tyr Lys					
	415		420		425	
	aaa aca cat aat cct atg gat gtc gca ggt ggt tgg aca gtt ggt ggg					1347
	Lys Thr His Asn Pro Met Asp Val Ala Gly Gly Trp Thr Val Gly Gly					
	430		435		440	
	tat aaa act cca gct cca tca gta act gaa ctt ggt atg gct cag ata					1395
	Tyr Lys Thr Pro Ala Pro Ser Val Thr Glu Leu Gly Met Ala Gln Ile					
	445		450		455	460

ttg gaa aat cct gct ggg gta atg cca caa tat tat ttt ggt aac cct	1443
Leu Glu Asn Pro Ala Gly Val Met Pro Gln Tyr Tyr Phe Gly Asn Pro	
465 470 475	
aac tat gat aac aca gtt cca cag agt cca cca tat gta tat aaa aat	1491
Asn Tyr Asp Asn Thr Val Pro Gln Ser Pro Pro Tyr Val Tyr Lys Asn	
480 485 490	
gaa gct tct tat cag gct gca tat aag act gca tta act gcc gca ggt	1539
Glu Ala Ser Tyr Gln Ala Ala Tyr Lys Thr Ala Leu Thr Ala Ala Gly	
495 500 505	
ggt acc gca gct gac att aaa aag gaa cat tgg cct cat aat gct gca	1587
Gly Thr Ala Ala Asp Ile Lys Lys Glu His Trp Pro His Asn Ala Ala	
510 515 520	
tca ggt ata tta gaa gct aat gat cca cca aat gtt aaa gac tta gct	1635
Ser Gly Ile Leu Glu Ala Asn Asp Pro Pro Asn Val Lys Asp Leu Ala	
525 530 535 540	
aat atg aat gga aca cca aac cgc tta tca aat gcg ttt act aac tat	1683
Asn Met Asn Gly Thr Pro Asn Arg Leu Ser Asn Ala Phe Thr Asn Tyr	
545 550 555	
gca ggt ggt agc tct aca aaa tct gca agt caa aat ggt tat ggt ttt	1731
Ala Gly Gly Ser Ser Thr Lys Ser Ala Ser Gln Asn Gly Tyr Gly Phe	
560 565 570	
ggt gat tta atg aac tat agt gta aat gct gag gga gtg tta ttt gga	1779
Gly Asp Leu Met Asn Tyr Ser Val Asn Ala Glu Gly Val Leu Phe Gly	
575 580 585	
gta tat tca aat gga gta caa ctt cca tta tat caa gta gct ctt tat	1827
Val Tyr Ser Asn Gly Val Gln Leu Pro Leu Tyr Gln Val Ala Leu Tyr	
590 595 600	
gat ttt aac tct aaa cag ggg tta cgt cgt gaa ggt ggt aac tta ttt	1875
Asp Phe Asn Ser Lys Gln Gly Leu Arg Arg Glu Gly Gly Asn Leu Phe	
605 610 615 620	
agt caa aca aga gaa tca ggg gac cca tct tca ggt gct gca aac act	1923
Ser Gln Thr Arg Glu Ser Gly Asp Pro Ser Ser Gly Ala Ala Asn Thr	
625 630 635	
tct ggg ttt ggt tca att aac gct aat act tta gaa gga tca aac gta	1971
Ser Gly Phe Gly Ser Ile Asn Ala Asn Thr Leu Glu Gly Ser Asn Val	
640 645 650	
gat ata tct aca gag ttt gtc tca atg att gca aca caa cgt gga ttc	2019
Asp Ile Ser Thr Glu Phe Val Ser Met Ile Ala Thr Gln Arg Gly Phe	
655 660 665	
cag tca aat agt aaa att gta act act att gac caa atg tta gag aca	2067
Gln Ser Asn Ser Lys Ile Val Thr Thr Ile Asp Gln Met Leu Glu Thr	
670 675 680	

gtt gta aat atg aag cgt tag 2088
Val Val Asn Met Lys Arg
685 690

<210> 2
<211> 690
<212> PRT
<213> Lawsonia intracellularis

<400> 2

Met Ser Leu Thr Ala Gly Met Trp Thr Gly Val Ser Gly Leu Leu Ser
1 5 10 15

His Gly Glu Lys Met Asn Val Ile Gly Asn Asn Ile Ala Asn Val Asn
20 25 30

Thr Val Gly Phe Lys Gly Gln Arg Met Asp Phe Ala Asp Phe Ile Tyr
35 40 45

Gln Asp Gly Phe Ser Thr Ala Gly Ile Thr Gln Ile Gly Arg Gly Val
50 55 60

Gly Ile Gly Ala Val Met Gly Asn Phe Gly Gln Gly Ser Phe Glu Thr
65 70 75 80

Thr Thr Glu Ala Thr Asp Leu Ala Ile Gly Gly Arg Gly Phe Phe Lys
85 90 95

Val Lys Pro Gln Gly Ser Glu Thr Ser Tyr Tyr Thr Arg Ala Gly Asn
100 105 110

Phe Arg Phe Asn Asn Asp Gly Tyr Leu Val Asp Pro His Gly Tyr Ala
115 120 125

Leu Gln Gly Trp Lys Ile Asp Asn Thr Glu Gly Pro Gln Arg Ile Ser
130 135 140

Gly Gly Val Asn Pro Gly Thr Asn Thr Ser Gln Ile Met Gly Thr Gly
145 150 155 160

Glu Pro Thr Asp Ile Arg Leu Asp Thr Trp Thr Val Ala Pro Leu Gln
165 170 175

Thr Thr Asn Val Ser Phe Asn Val Asn Leu Ser Ser Asp Lys Ser Gly

			180					185						190			
Asp	Lys	Ser	Gln	Asn	Val	Asn	Ser	Pro	Phe	Thr	Ser	Leu	Phe	Asn	Ile		
		195					200					205					
Trp	Asn	Gly	Lys	Gln	Pro	Ser	Glu	Pro	Asn	Asn	Pro	Pro	Met	Pro	Glu		
	210					215					220						
Ser	Ala	Tyr	Ser	Tyr	Gln	Thr	Ser	Ile	Lys	Val	Tyr	Asp	Glu	Ala	Gly		
225					230					235					240		
Gly	Thr	His	Thr	Leu	Thr	Val	Tyr	Phe	Asp	Gln	Val	Ser	Pro	Lys	Asp		
				245					250					255			
Tyr	Lys	Gly	Gly	Gly	Ser	Gly	Glu	Ser	Val	Trp	Glu	Tyr	Val	Val	Thr		
			260					265					270				
Met	Asp	Pro	Ser	Glu	Asp	Asn	Arg	Gln	Val	Ser	Val	Gly	Gly	Asn	Ile		
		275					280					285					
Val	Asp	Ile	Lys	Asp	Thr	Lys	Ala	Ala	Gly	Met	Leu	Met	Ser	Gly	Thr		
		290				295					300						
Leu	Ser	Phe	Asp	Ser	Ser	Gly	Lys	Leu	Ala	Asn	Gln	Ser	Ala	Tyr	Ser		
305					310					315					320		
Leu	Asn	Gly	Ser	Arg	Lys	Pro	Ala	Val	Asp	Pro	Ala	Thr	Gly	Ala	Leu		
				325					330				335				
Ile	Asn	Gly	Asn	Gly	Phe	Thr	Ile	Asp	Arg	Asp	Gly	Asn	Ala	Ile	Pro		
			340					345					350				
Ile	Leu	Asn	Ile	Asp	Asn	Pro	Ala	Glu	Asn	Phe	Tyr	Pro	Ala	Glu	Val		
		355					360					365					
Ser	Asn	Asn	Gly	Phe	Pro	Met	Ile	Val	Ala	Asn	Phe	Thr	Gly	Val	Pro		
		370				375					380						
Gly	Lys	Asn	Thr	Ala	Gly	Ser	Val	Gly	Asp	Ala	Thr	Thr	Phe	Phe	Thr		
385					390				395						400		
Glu	Ile	Asp	Phe	Gly	Leu	Lys	Ala	Thr	Asp	Leu	Asp	Asn	Thr	Trp	Lys		
			405						410					415			

Asn Ala Asn Glu Pro Leu Ser Ser Leu Ser Tyr Lys Lys Thr His Asn
420 425 430

Pro Met Asp Val Ala Gly Gly Trp Thr Val Gly Gly Tyr Lys Thr Pro
435 440 445

Ala Pro Ser Val Thr Glu Leu Gly Met Ala Gln Ile Leu Glu Asn Pro
450 455 460

Ala Gly Val Met Pro Gln Tyr Tyr Phe Gly Asn Pro Asn Tyr Asp Asn
465 470 475 480

Thr Val Pro Gln Ser Pro Pro Tyr Val Tyr Lys Asn Glu Ala Ser Tyr
485 490 495

Gln Ala Ala Tyr Lys Thr Ala Leu Thr Ala Ala Gly Gly Thr Ala Ala
500 505 510

Asp Ile Lys Lys Glu His Trp Pro His Asn Ala Ala Ser Gly Ile Leu
515 520 525

Glu Ala Asn Asp Pro Pro Asn Val Lys Asp Leu Ala Asn Met Asn Gly
530 535 540

Thr Pro Asn Arg Leu Ser Asn Ala Phe Thr Asn Tyr Ala Gly Gly Ser
545 550 555 560

Ser Thr Lys Ser Ala Ser Gln Asn Gly Tyr Gly Phe Gly Asp Leu Met
565 570 575

Asn Tyr Ser Val Asn Ala Glu Gly Val Leu Phe Gly Val Tyr Ser Asn
580 585 590

Gly Val Gln Leu Pro Leu Tyr Gln Val Ala Leu Tyr Asp Phe Asn Ser
595 600 605

Lys Gln Gly Leu Arg Arg Glu Gly Gly Asn Leu Phe Ser Gln Thr Arg
610 615 620

Glu Ser Gly Asp Pro Ser Ser Gly Ala Ala Asn Thr Ser Gly Phe Gly
625 630 635 640

Ser Ile Asn Ala Asn Thr Leu Glu Gly Ser Asn Val Asp Ile Ser Thr
645 650 655

Glu Phe Val Ser Met Ile Ala Thr Gln Arg Gly Phe Gln Ser Asn Ser
660 665 670

Lys Ile Val Thr Thr Ile Asp Gln Met Leu Glu Thr Val Val Asn Met
675 680 685

Lys Arg
690

<210> 3
<211> 751
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (32)..(715)

<400> 3
aagagttacc ctagcgttag gagctaacaa c atg ttt cgt atg att gtt ttt 52
Met Phe Arg Met Ile Val Phe
1 5

ttt act gta ggt atc att atg ctt att ctt gct tgc tta gct gca ctt 100
Phe Thr Val Gly Ile Ile Met Leu Ile Leu Ala Cys Leu Ala Ala Leu
10 15 20

gag ttc ata caa gat ttt ccc aat agc tat caa gaa gat gga caa atg 148
Glu Phe Ile Gln Asp Phe Pro Asn Ser Tyr Gln Glu Asp Gly Gln Met
25 30 35

gtt aca gga att att tca aaa ata ata ggc tct aac tgt gat aat tct 196
Val Thr Gly Ile Ile Ser Lys Ile Ile Gly Ser Asn Cys Asp Asn Ser
40 45 50 55

tca aca tct gat ata aat aat aag aaa tcc ata gat aga gat aaa gat 244
Ser Thr Ser Asp Ile Asn Asn Lys Lys Ser Ile Asp Arg Asp Lys Asp
60 65 70

aca tta ctc tca agt agt aat aga aat aca ata caa gcc ggt act cca 292
Thr Leu Leu Ser Ser Ser Asn Arg Asn Thr Ile Gln Ala Gly Thr Pro
75 80 85

cat ca